

<110> CuraGen Corporation et al.
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Eichen, Joseph
Lepley, Denise M.
Miller, Charles E.
Mezes, Peter
Hahne, William

<120> COMPOSITIONS AND METHODS OF USE FOR A FIBROBLAST GROWTH FACTOR

<130> Cura-57 SNP

<140> ***Enter Current Patent Application ID***

<141> 2004-11-3

<150> 10/702,126

<151> 2003-11-4

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<170> CuraSeqList version 0.1

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 Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile
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 Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu
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 Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr
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Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu
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cgc cgc cgg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg 144
Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
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Pro Asp Gly Ser Ala Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
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Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
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Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu

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Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
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Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
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Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
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Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
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Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
 130 135 140

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tct ggc ctg tac ctg ggt atg aac gac aaa ggc gaa ctg tac ggt tct				384
Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser				
115	120	125		
gaa aaa ctg acc tct gaa tgc atc ttc cgt gaa cag ttt gaa gag aac				432
Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn				
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Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly				
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Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro				
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Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His			
165	170	175	
cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt gtt		576	
Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val			
180	185	190	
cca gaa ctg tat aaa aac ctg ctg atg tac acc taa		612	
Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr			
195	200		
<210> 15			
<211> 203			
<212> PRT			
<213> Homo sapiens			
<400> 15			
Gly Phe Leu Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His			
1	5	10	15
Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg			
20	25	30	
Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln			
35	40	45	
Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg			
50	55	60	
Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr			
65	70	75	80
Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala			
85	90	95	
Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly			
100	105	110	
Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu			
115	120	125	
Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser			

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130

135

140

Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala
 145 150 155 160

Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His
 165 170 175

Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val
 180 185 190

Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr
 195 200

<210> 16

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(600)

<400> 16

ggc ggt ctg gag ggt ctg ggt cag cag gtt ggt tct cac ttc ctg ctg 48
 Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu
 1 5 10 15

ccg ccg gct ggt gaa cgt ccg cca ctg ctg ggt gaa cgt cgc tcc gca 96
 Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala
 20 25 30

gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct cag ctg gct cac 144
 Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His
 35 40 45

ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc cgt act ggt ttc 192
 Leu His Gly Ile Leu Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe
 50 55 60

cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt acc cgt cag gac 240
 His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp
 65 70 75 80

cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt gct gtt ggt ctg 288
 His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu
 85 90 95

gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg ggt atg aac gac 336
 Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp
 100 105 110

aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct gaa tgc atc ttc 384
 Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe
 115 120 125

cgt gaa cag ttt gaa gag aac tgg tac aac acc tac tct tcc aac atc 432
 Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile
 130 135 140

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tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt gct ctg aac aaa		480
Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys		
145 150 155 160		
gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt cac cag aaa ttc		528
Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe		
165 170 175		
acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt gtt cca gaa ctg		576
Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu		
180 185 190		
tat aaa aac ctg ctg atg tac acc taa		603
Tyr Lys Asn Leu Leu Met Tyr Thr		
195 200		
<210> 17		
<211> 200		
<212> PRT		
<213> Homo sapiens		
<400> 17		
Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu		
1 5 10 15		
Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala		
20 25 30		
Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His		
35 40 45		
Leu His Gly Ile Leu Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe		
50 55 60		
His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp		
65 70 75 80		
His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu		
85 90 95		
Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp		
100 105 110		
Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe		
115 120 125		
Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile		
130 135 140		
Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys		
145 150 155 160		
Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe		
165 170 175		
Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu		
180 185 190		
Tyr Lys Asn Leu Leu Met Tyr Thr		
195 200		

<210> 18
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(591)

<400> 18

gag ggt ctg ggt cag cag gtt ggt tct cac ttc ctg ctg ccg ccg gct	48
Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala	
1 5 10 15	

ggt gaa cgt ccg cca ctg ctg ggt gaa cgt cgc tcc gca gct gaa cgc	96
Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg	
20 25 30	

tcc gct cgt ggt ggc ccg ggt gct gct cag ctg gct cac ctg cat ggt	144
Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly	
35 40 45	

atc ctg cgt cgc cgt cag ctg tac tgc cgt act ggt ttc cac ctg cag	192
Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln	
50 55 60	

atc ctg ccg gat ggt tct gtt cag ggt acc cgt cag gac cac tct ctg	240
Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu	
65 70 75 80	

ttc ggt atc ctg gaa ttc atc tct gtt gct gtt ggt ctg gtt tct atc	288
Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile	
85 90 95	

cgt ggt gtt gac tct ggc ctg tac ctg ggt atg aac gac aaa ggc gaa	336
Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu	
100 105 110	

ctg tac ggt tct gaa aaa ctg acc tct gaa tgc atc ttc cgt gaa cag	384
Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln	
115 120 125	

ttt gaa gag aac tgg tac aac acc tac tct tcc aac atc tac aaa cat	432
Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His	
130 135 140	

ggt gac acc ggc cgt cgc tac ttc gtt gct ctg aac aaa gac ggt acc	480
Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr	
145 150 155 160	

ccg cgt gat ggt gct cgt tct aaa cgt cac cag aaa ttc acc cac ttc	528
Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe	
165 170 175	

ctg ccg cgc cca gtt gac ccg gag cgt gtt cca gaa ctg tat aaa aac	576
Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn	
180 185 190	

ctg ctg atg tac acc taa

Leu Leu Met Tyr Thr
195

<210> 19

<211> 197

<212> PRT

<213> Homo sapiens

<400> 19

Glu	Gly	Leu	Gly	Gln	Gln	Val	Gly	Ser	His	Phe	Leu	Leu	Pro	Pro	Ala
1				5					10				15		

Gly	Glu	Arg	Pro	Pro	Ieu	Leu	Gly	Glu	Arg	Arg	Ser	Ala	Ala	Glu	Arg
					20			25				30			

Ser	Ala	Arg	Gly	Gly	Pro	Gly	Ala	Ala	Gln	Leu	Ala	His	Leu	His	Gly
					35			40			45				

Ile	Leu	Arg	Arg	Arg	Gln	Leu	Tyr	Cys	Arg	Thr	Gly	Phe	His	Leu	Gln
					50			55			60				

Ile	Leu	Pro	Asp	Gly	Ser	Val	Gln	Gly	Thr	Arg	Gln	Asp	His	Ser	Leu
					65			70		75		80			

Phe	Gly	Ile	Leu	Glu	Phe	Ile	Ser	Val	Ala	Val	Gly	Leu	Val	Ser	Ile
					85			90			95				

Arg	Gly	Val	Asp	Ser	Gly	Leu	Tyr	Leu	Gly	Met	Asn	Asp	Lys	Gly	Glu
					100			105			110				

Leu	Tyr	Gly	Ser	Glu	Lys	Leu	Thr	Ser	Glu	Cys	Ile	Phe	Arg	Glu	Gln
					115			120			125				

Phe	Glu	Glu	Asn	Trp	Tyr	Asn	Thr	Tyr	Ser	Ser	Asn	Ile	Tyr	Lys	His
					130			135			140				

Gly	Asp	Thr	Gly	Arg	Arg	Tyr	Phe	Val	Ala	Leu	Asn	Lys	Asp	Gly	Thr
					145			150		155		160			

Pro	Arg	Asp	Gly	Ala	Arg	Ser	Lys	Arg	His	Gln	Lys	Phe	Thr	His	Phe
					165			170			175				

Leu	Pro	Arg	Pro	Val	Asp	Pro	Glu	Arg	Val	Pro	Glu	Leu	Tyr	Lys	Asn
					180			185			190				

Leu Leu Met Tyr Thr
195

<210> 20

<211> 567

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(564)

<400> 20

cac	ttc	ctg	ctg	ccg	ccg	gct	ggt	gaa	cgt	ccg	cca	ctg	ctg	ggt	gaa

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1	5	10	15	
cgt cgc tcc gca gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct				96
Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala				
20	25	30		
cag ctg gct cac ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc				144
Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Gln Leu Tyr Cys				
35	40	45		
cgt act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt				192
Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly				
50	55	60		
acc cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt				240
Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val				
65	70	75	80	
gct gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg				288
Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu				
85	90	95		
ggg atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct				336
Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser				
100	105	110		
gaa tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac acc tac				384
Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr				
115	120	125		
tct tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt				432
Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val				
130	135	140		
gct ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt				480
Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg				
145	150	155	160	
cac cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt				528
His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg				
165	170	175		
gtt cca gaa ctg tat aaa aac ctg ctg atg tac acc taa				567
Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr				
, 180	185			
<210> 21				
<211> 188				
<212> PRT				
<213> Homo sapiens				
<400> 21				
His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu				
1	5	10	15	
Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala				
20	25	30		
Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys				
35	40	45		

Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly
 50 55 60

Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val
 65 70 75 80

Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu
 85 90 95

Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser
 100 105 110

Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr
 115 120 125

Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val
 130 135 140

Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg
 145 150 155 160

His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg
 165 170 175

Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr
 180 185

<210> 22

<211> 447

<212> DNA

<213> Homo sapiens

<400> 22

atcctgcgcc gccggcagct ctattgccgc accggcttcc acctgcagat cctgcccac 60
 ggcagcgtgc agggcacccg gcaggaccac agcctttcg gtatcttggaa attcatcagt 120
 gtggcagttgg gactggtcag tattagaggt gtggacagtg gtctctatct tggaaatgaat 180
 gacaaaggag aactctatgg atcagagaaa cttacttccg aatgcattt tagggagcag 240
 tttgaagaga actgtataa cacctattca tctaacaatat ataaaacatgg agacactggc 300
 cgcaggtatt ttgtggact taacaaagac ggaactccaa gagatggcgc caggtccaag 360
 aggcatcaga aatttacaca tttcttacct agaccagtgg atccagaaaa agttccagaa 420
 ttgtacaagg acctactgtat gtacact 447

<210> 23

<211> 149

<212> PRT

<213> Homo sapiens

<400> 23

Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln
 1 5 10 15

Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu
 20 25 30

Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile
 35 40 45

Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu
 50 55 60

Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln
65 70 75 80

Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His
85 90 95

Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr
100 105 110

Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe
115 120 125

Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn
130 135 140

Leu Leu Met Tyr Thr
145

<210> 24

<211> 537

<212> DNA

<213> Homo sapiens

<400> 24

atggctccct tagccgaagt cggggccttt ctgggcggcc tggagggctt gggccagccg 60
ggggcagcgc agctggcgca cctgcacggc atcctgcgcc gccggcagct ctattgccgc 120
accggcttcc acotgcagat cctgcccgc ggcagcgtgc agggcacccg gcaggaccac 180
agccctctcg gtatcttggaa attcatcagt gtggcagtgg gactggtcag tatttagaggt 240
gtggacagtg gtctctatct tggaatgaat gacaaaggag aactctatgg atcagagaaa 300
cttacttccg aatgcatctt tagggagcag tttgaagaga actgtataa cacctattca 360
tctaacaatat ataaacatgg agacactggc cgcaggtatt ttgtggcact taacaaagac 420
ggaactcaa gagatggcgc caggtccaag aggcatcaga aatttacaca tttctiacct 480
agaccagtgg atccagaaag agttccagaa ttgtacaaga acctactgtat gtacact 537